Strain	Treatment	Elongation Rate (bp/s)[a]	ppGpp/GTP[b]	pppGpp/GTP[b]	ppGpp/ATP[b]	pppGpp/ATP[b]	GTP/ATP[b]
*dnaC*2	Untreated	651±23	0.003±0.03	0.0002±0.03	0.016±0.01	0.008±0.02	0.602±0.03
	SHX	565±27	2.29±0.23	0.72±0.17	0.61±0.08	0.20±0.04	0.29±0.03
*dnaC*2 Δ*gppA*	Untreated	621±14	0.05±0.02	0.05±0.02	0.02±0.01	0.03±0.01	0.55±0.05
	SHX	403±21	2.41±0.21	2.43±0.24	0.55±0.05	0.57±0.09	0.24±0.04
*dnaC*2 pRelA*	Untreated	592±12	0.15±0.03	0.18±0.04	0.08±0.02	0.07±0.06	0.51±0.03
	IPTG	503±24	1.19±0.03	0.51±0.13	0.55±0.06	0.14±0.05	0.46±0.02
*dnaC*2 Δ*gppA* pRelA*	Untreated	604±17	0.15±0.03	0.18±0.06	0.08±0.01	0.07±0.06	0.56±0.04
	IPTG	386±12	1.33±0.06	1.16±0.03	0.59±0.02	0.50±0.04	0.43±0.02

[a] ±Range
[b] ±SEM

Table S1. Replication elongation rates and nucleotide levels in *E. coli* following induction of (p)ppGpp.

Cells were treated with SHX (0.5 mg/ml) or treated with IPTG (1 mM) to induce expression of RelA*. Replication rates were calculated by linear regression of a time course of the average replication fork positions generated by genomic microarrays. Nucleotide levels were determined by TLC and shown as molar ratios of the indicated nucleotide.

Strain	Treatment	% Replication (treated/t0)	ppGpp/GTP	pppGpp/GTP	ppGpp/ATP	pppGpp/ATP	GTP/ATP
$P_{hyperspank}$	Untreated	127±5	0.004±0.08	0.01±0.007	0.002±0.02	0.01±0.002	0.63±0.03
	Norv	36±2	0.18±0.004	0.17±0.08	0.01±0.001	0.01±0.001	0.45±0.004
	α-MG	20±1	0.41±0.05	0.37±0.02	0.08±0.01	0.07±0.004	0.47±0.01
	RHX	4±1	0.48±0.03	1.93±0.18	0.07±0.0001	0.27±0.006	0.11±0.01
$P_{hyperspank}$-*gppA*	Untreated	106±12	0.02±0.01	0.02±0.02	0.002±0.001	0.02±0.008	0.55±0.01
	Norv	32±3	0.45±0.12	0.62±0.07	0.02±0.001	0.02±0.005	0.38±0.01
	α-MG	12±2	1.13±0.21	1.22±0.09	0.03±0.001	0.12±0.017	0.12±0.03
	RHX	6±1	1.26±0.21	1.55±0.31	0.18±0.02	0.16±0.014	0.10±0.01

Table S2. Relative replication rates and nucleotide levels in *B. subtilis* following induction of (p)ppGpp.

Cells were treated with 0.5 mg/ml norvaline (Norv), 2% α-methyl-glucoside (α-MG), and 0.5 mg/ml RHX. The relative rate of DNA replication is shown as the rate of incorporation of ^{3}H-thymidine into DNA and expressed as a percentage of t0. Nucleotide levels were determined by TLC and shown as molar ratios of the indicated nucleotide. Error indicates SEM.

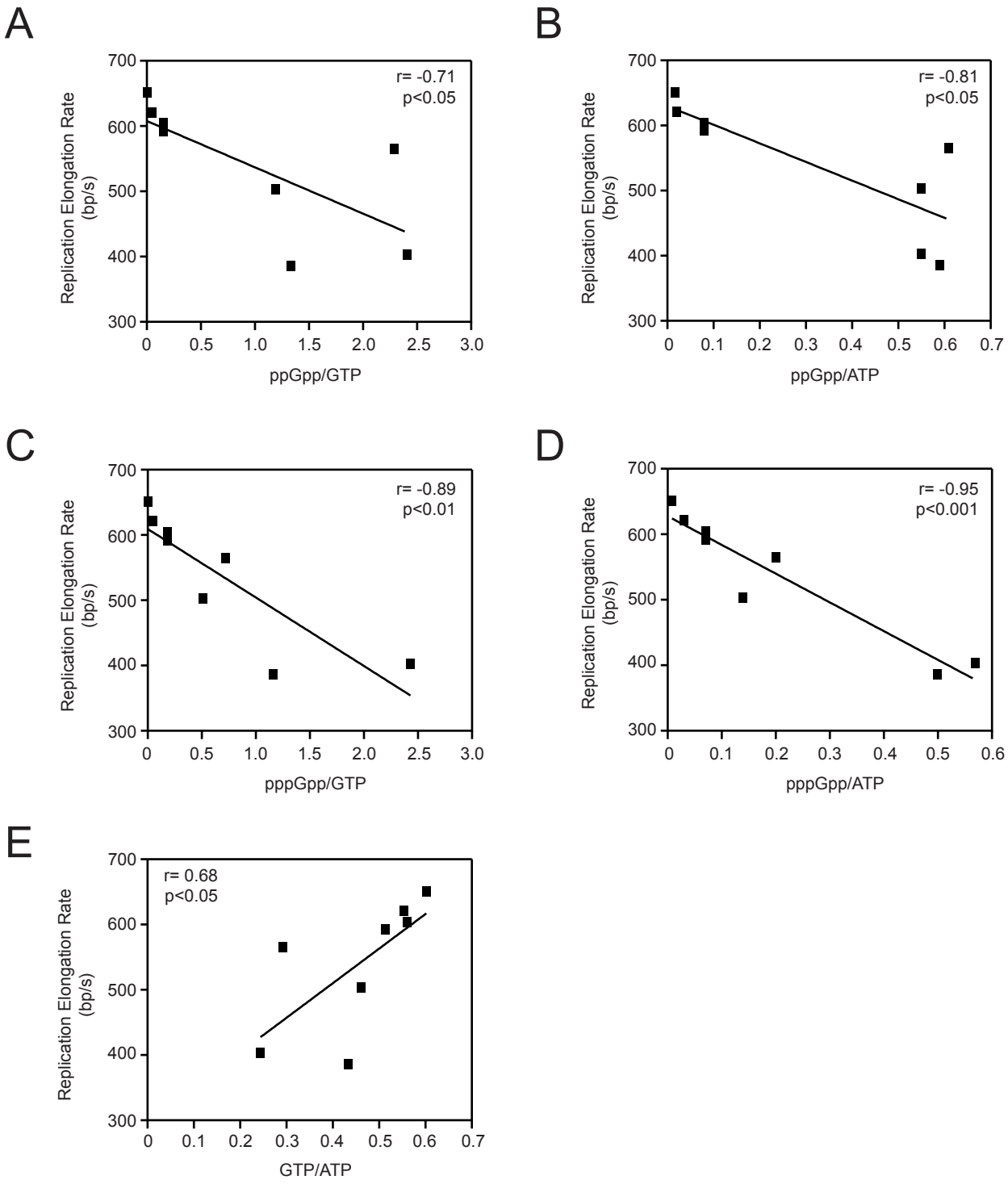

Figure S1. Replication elongation rates in *E. coli* relative to nucleotide levels under (p)ppGpp-inducing conditions.

Replication elongation rates (Table S1) were plotted against nucleotide levels presented as the molar ratio of the indicated nucleotide (Table S1). (A) ppGpp/GTP, (B) ppGpp/ATP, (C) pppGpp/GTP, (D) pppGpp/ATP, and (E) GTP/ATP. Data were fit by linear regression. r: Pearson's correlation coefficient.

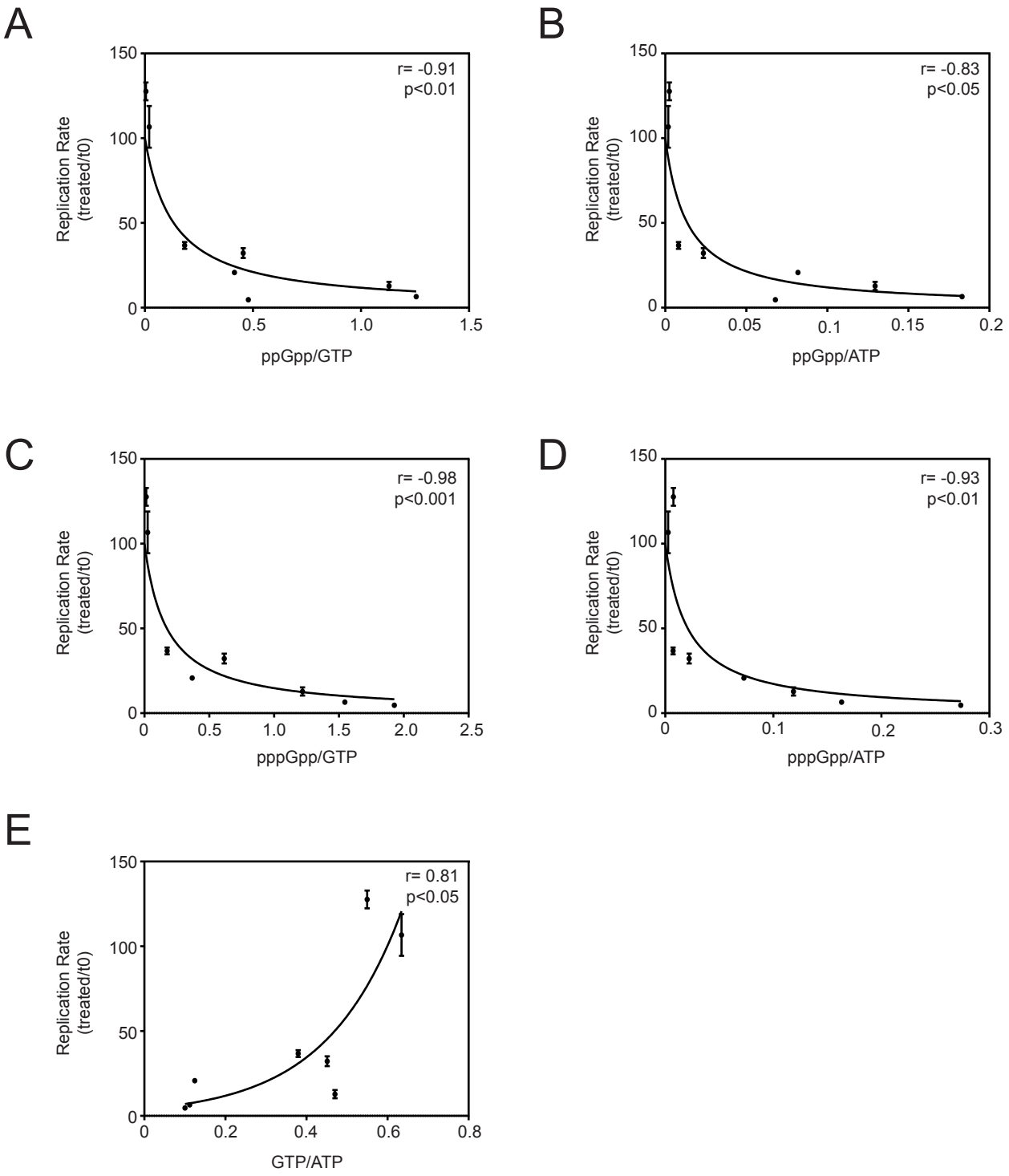

Figure S2. Replication elongation rates in *B. subtilis* relative to nucleotide levels under (p)ppGpp-inducing conditions.

Replication rates (Table S2) were plotted against nucleotide levels presented as the molar ratio of the indicated nucleotide (Table S2). (A) ppGpp/GTP, (B) ppGpp/ATP, (C) pppGpp/GTP, (D) pppGpp/ATP, and (E) GTP/ATP. (A-D) Data were fit to y=100/(1+(x/IC50)) where y is the replication rate, and x is the relative (p)ppGpp level. (E) Data were fit via exponential growth. r: Spearman's rank correlation coefficient.